

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 30, 2001, 04:14:06 ; Search time 1386.2 Seconds
(without alignments)
11790.495 Million cell updates/sec

Title: US-09-403-262A-1
Perfect score: 1729
Sequence: 1 cctcgtccctcccccag.....ctattttattttaatta 1729

Scoring table: IDENTITY_NTC
Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
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258: gb_est189:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

QY	969	ttttgcatagggtttaagtcgaatgaacccaataatggttacatccgagaaagaagca	1028
Db	95	ttttggaattggtgaagtcctctctcctcctaaagtgtgaccccttgtagcaaatca	154
QY	1029	atcatbaccatcccttttttttcaaaagtatcatcgagcggttgatattatatacgcg	1088
Db	155	ACACAAACACAAACACCTTTCTTCACAGGTCATAGAAACTCTAGACTACTACTGGCA	214
QY	1089	tgtttattactgaagctacacattgcagcgagtcgagagagataacagttgac	1148
Db	215	TCCTGAGTCATCGATGTCACCCCTCTCAAGAAATACGAAGAGATTAAGTGGAC	274
QY	1149	aagtggtgtttggagagagatggttgatcgtttgcgtatggaagagataaaagaag	1208
Db	275	ACACTGTTTGGCTCGGGATATCTCAATGTCTATGCTGTGAAGCAAAAGAAAGGCTGC	334
QY	1209	aaagacatgaaaggtttagatcatcagtgaaagtatgtatgagagttctgattagtaab	1268
Db	335	AGCGACACCAACTGTTTGTGAAGGAAGCTCAGGTATACATGCGCGGATTTTCGCAAT	394
QY	1269	tgtctttaagccctttgacatcacaaagctaacctctcttttagagctcatatccct	1328
Db	395	GTCCTTTGAGTCTTATGTGAATTTCTGTTATGAAGAGCTTCTAG- - - - -TGTATT	448

/organism="Glycine max"
 /db_xref="taxon:3847"
 /clone="Gm-r1070-7269"
 /clone_1bp="Gm-r1070"
 /note="The library Gm-r1070 is a sequence-driven, retracked
 set of 9,216 clones selected from cDNA libraries from
 various tissues and stages of development of soybean tha
 represent 2,639 sequences from immature cotyledons, 1,777
 from immature seed coats, 3,938 from flowers, and 869
 from young pods. The 5' ESTs of the source clones from
 the different libraries was used to select singletons, o
 a representative of each contig, which were retracked
 from library Gm-r1070. The cDNA clones of the retracked
 Gm-r1070 library were then sequenced at the 3' end. The
 contig analysis to select unique genes was performed by
 the laboratory of Ernest Reitzel, Center for Computational
 Genomics and Bioinformatics, University of Minnesota.
 http://www.cbc.umn.edu/Research/Projects/Soybean/index.htm
 . Retracking was performed by Genome Systems, St. Louis,
 http://www.genomesystems.com, and 3' sequencing by the
 Reck Center for Comparative and Functional Genomics,
 University of Illinois,
 http://www.illife.uiuc.edu/biotech/reck.html. Note: The
 corresponding 5' EST from each clone in the Gm-r1070
 library is listed in the OTHER EST field. The detailed
 information on the source library for each clone can also
 be obtained by referring to the genome systems clone ID o


```

/clone="PMHRP-57C20"
/clone_lib="MHRP-n"
/tissue_type="roots"
/dev_stage="phosphate-starved"
/lab_host="XLOLR"
/notes="Vector: Bluescript SK-, Site_1: EcoRI; Site_2:
XhoI; At the trifoliolate stage, M. truncatula plants were
transplanted to phosphate-free sand and grown for a
further 30 days. During this period, they were fertilized
twice weekly with 1/2 Hoaglands solutions containing 200mM
potassium phosphate. cDNA was prepared from polyA+
enriched RNA. The cDNA was directionally ligated into the
Unizap XR vector from Stratagene and packaged using
Gigapack III Gold packaging extracts. Plasmids containing
cDNA inserts were excised from the recombinant lambda-zap
phage using Ex-assist helper phage and propagated in
XLOLR cells."

```

Query Match	6.2%	Score 107.2	DB 155	Length 772
Best Local Similarity	60.1%	Prod. No. 7.6e-15		
Matches 178	Conservative	0	Mismatches 118	Indels 0
				Gaps 0
Qy 969	tttgcattagaggttaagcatgacatgacccctaagaattgttacaatcgcgaggaagacaa	1028		
Db 63	ttctccgcattggttttagagccttatcccaaaactgttgaacgtttggaaacagactga	122		
Qy 1029	atcataaccatcccttttttacaagaattcatcgagcgcttgattatatacagctg	1088		
Db 123	acacaaacacttccccatttctccaaacattgttgaaaccttacaattactactgcgcg	182		
Qy 1089	tgtttattcacttggaagctacatctgcaccgcggtagtgcgagagagatgacagttgaac	1148		
Db 183	tgttttagtgcctttagacgcacactcttccgagagagacgacaagatagaggtgaattggaaa	242		
Qy 1149	aagtgtcgatttgaggagagagattgtgatatcgtttgcgattggaagagagataaagaag	1208		
Db 243	ggcaaatgcttggcggagagacatttgaaatgcatattgcttgcgagggcgcagatrgaatag	302		
Qy 1209	aaggaactgaaaggttttagatcatctggaaagtatgttagagagtttgattagttagt	1264		
Db 303	aaagatgtgaatgccttgcaaaatgagagcgcaagatgaaatggcttgatttcact	358		

RESULT	6	EST	15-MAR-2001
LOCUS	BG443698	671 bp	mRNA
DEFINITION	GA_Ea0021L107f Gossypium arboreum 7-10 dpa fiber library Gossypium		
ACCESSION	BG443698		
VERSION	BG443698		
KEYWORDS	BG443698.1 GI:13353350		
SOURCE	EST.		
ORGANISM	Gossypium arboreum.		
	Gossypium arboreum.		
	Eukaryotes: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;		
	Rosidae; eustosids II; Malvales; Malvaceae; Gossypium.		
REFERENCE	1 (bases 1 to 671)		
AUTHORS	Wing, R.A., Frisch, D., Yu, Y., Main, D., Rambo, T., Simmons, J., Henry		
	, D., Wood, T.C., Leslie, A. and Wilkins, T.A.		
TITLE	An integrated analysis of the genetics, development, and evolution		
	of the cotton fiber		
JOURNAL	Unpublished (2000)		
COMMENT	Contact: Wing RA		
	Clemson University Genomics Institute		
	Clemson University		
	100 Jordan Hall, Clemson, SC 29634, USA		
	Tel: 864 656 7288		
	Fax: 864 656 4293		
	Email: twinge@clemson.edu		
	Seq primer: TATACGACTCATTATAGCG		

```

FEATURES
    source
        High quality sequence stop: 465.
        Location/Qualifiers
            1..671
                /organism="Gossypium arboreum"
                /strain="AKA"
                /cultivar="8400"
                /db_xref="taxon:29729"
                /clone="GA_Ea0021L07f"
                /clone_lib="Gossypium arboreum 7-10 dpa fiber library"
                /tissue_type="Fibers isolated from bolls harvested 7-10
                dpa"
                /lab_host="E. coli"
                /note="vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"
BASE COUNT
    153 a      122 c      221 g      175 t
ORIGIN

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Query Match	Best Local	Similarity	Score	DB	Length
Matches	259;	Conservative	50.4%;	Pred. No. 1.4e-14;	Mismatches 259; Indels 0; Caps 0;
OY	898	tgaacccctgcatcacaactggtgtttcttaccctccacccgctctttaaagaccgcgaaaa	957		
DB	1	TGAAGTACTAGCCGGTGAAGCGCTGTTTCAGAGCTTCATCCCTTGTTAGCTCGACCGGGTGG	60		
OY	958	gttaagagttttttgcatagggtttaagtaacaaagccctaataattgttaccatccgga	1017		
DB	61	GATGCAAAAAGTTTTCCTCTATTAAGCGATGAACCCAGATTTGTCACGGTTGTGA	120		
OY	1018	gaaggaagcaaatcatataaccatccctcttttttacaagaatcattcagagcggttgatta	1077		
DB	121	ACAAAGAACGATCAACAAACGGCTCTGTTTCTTAAACCGTTTAACTGAAGCTCTCCATTA	180		
OY	1078	ttatacagctgtgtttgatttaccgsgaagttlaattgcccacgsgtagtcgagagagant	1137		
DB	181	TATATCTTAACCTTTTCGACTCGTTGAGAGGTTGGGGGTGGGCCCAACGATCAAGACCT	240		
OY	1138	gacagttgacaacagtgtgtgttggagagagagattgttgatatacgtttgcagtggaagaga	1197		
DB	241	GCGTATGTCCGAGTATATCTTAGGAAGACAAATTTGTAACGTGGTGCCTGTGAAGGAT	300		
OY	1198	taaaagaaagaagaacatgaaagtttagtactcaggaagttatgtttgagagtttgg	1257		
DB	301	GGACCCAGTTGAGCGACACAGACGCCCTCACTACAGTGAAGAACTGGATGAAACGGCCGG	360		
OY	1258	atttagtaatgttgcctttaagccctttgcatattacacaagctaaactcttttagact	1317		
DB	361	GTTTACCCCTGTCATTGTGGTGTCCAAATGCTTATTAACAACTGATATGTTGGCCCT	420		
OY	1318	tcaattactcttgaagagcttaoactcagagtttcgtagtaattcttcttctaagtt	1377		
DB	421	CTTCCGCCAGCGCGGATGGGATATAGTGTGAGAGAGAAATATGGGTCTTTAATGCTTGGGTG	480		
OY	1378	gcaaatcaaacccctttctccatctcgtcttgg	1411		
DB	481	GCATACAAAGCCACTTATCGACACCTGAGAGTTGG	514		
RESULT	7				
AW726448		standard; RNA; EST; 679 BP.			
ID	AW726448				
XX	AC	AW726448;			
XX	SV	AW726448.1			
XX	SV	24-APR-2000 (Rel. 63, Created)			
DT	18-NOV-2000	(Rel. 65, Last updated, Version 2)			
DE	GA_Ea0021l07	Gossypium arboreum 7-10 dpa fiber library Gossypium arboreum			
DE	CDNA clone GA_Ea0021l07	mRNA sequence.			
XX	EST.				

```

XX Gossypium arboreum
OS Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Malvales; Malvaceae; Gossypium.
XX
XX [1]
XX 1-679
XX Wang R.A., Frisch D., Yu Y., Main D., Rambo T., Simmons J., Henry D.,
XX Wood T.C., Leslie A., Wilkins T.A.;
XX "An integrated analysis of the genetics, development, and evolution of the
XX cotton fiber";
XX unpublished.
XX
XX Contact: Ming RA
XX Clemson University Genomics Institute
XX 100 Jordan Hall, Clemson, SC 29634, USA
XX Tel: 864 656 7288
XX Fax: 864 656 4293
XX Email: rwing@clemson.edu
XX High quality sequence stop: 679.
XX
XX Key Location/Qualifiers
XX
XX source 1..679
XX /db_xref="taxon:29729"
XX /db_xref="ESTLIB:2480"
XX /note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"
XX /organism="Gossypium arboreum"
XX /strain="AKA"
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XX /clone="GA_Ea0021107"
XX /clone_id="Gossypium arboreum 7-10 dpa fiber library"
XX /tissue_type="Fibers isolated from bolls harvested 7-10
XX dpa"
XX /lab_host="E. coli"
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XX Sequence 679 BP; 155 A; 124 C; 225 G; 175 T; 0 other:

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```

Query Match 6.1%; Score 106; DB 76; Length 679;
Best Local Similarity 50.4%; Pred. No. 1.4e-14;
Matches 259; Conservative 0; Mismatches 255; Indels 0; Gaps 0;

Oy 898 tgaaacctagatcaactggttttctaccaccgacctttaaagaacgcgaaaa 957
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Db 9 TGAAGTAGTAGCGGAGACGCTGTTTCGAGCTTCATCCCTTGTTAGTCGACGCGGTG 68

Oy 958 gttaaagatttttgcctagaggttaagtcataagaccctaaattgttacaatcgcgga 1017
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 69 GATCGAAAAGTTGTTCTCTATTAAAGCGATGAACCAAGATTGTCACGGTTGTGA 128

Oy 1018 gaagaagaacaatcaacatcctcttctttaaagaattcatcgagcgcttgatga 1077
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 129 ACAAGAACCGATCAACAACGCTCGTTTCTTAAACCGTTTACTGAAGCTCTCCATTA 188

Oy 1078 ttatacagctgltgttgaatcaactggaagctacattgccaacgggttagtcgagaagagat 1137
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 189 TTAATTCACCTTTTCGACCTGTTTGGAAGGTTTCGGGGTGGCCGACGAGTCAAGACT 248

Oy 1138 gacagtgaaacaagtgtgttgagagagagatgtgtatcgttcgatagaagaga 1197
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Db 249 GCGATATGCCAGATTATCTTAGGAAGACAGATTGTAACTGTGCTTGTAAGAGGAT 308

Oy 1198 taaaaagaaagaacatacgaagtttagatcatcgggaagttatgttgaagagtg 1257
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 309 GGACCGAGTTGAGCGACACGAGCCGCTCAGTCAGTGGAGAACTCGATGGAACGCCGG 368

Oy 1258 attagtaatgttccttaagccctttagcatatcaacaagctaaagctctttagagat 1317
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 369 GTTAGCCCTGTTCATTTGGGTCCAAATGCTTAAACAAGTAACTAGTATGTTGGCCCT 428

```

```

Oy 1318 tcattaccctctgaagagctatacaactcgaggttcgagtaattcttctttagtg 1377
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 429 CTTCGCCACGCGCGATGGGTATAGAGTGGAGACAAATATAGGTATTATCTTTGGGTG 488

Oy 1378 gcaaatcaacccttctccatctgcttgg 1411
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 489 GCATPACAAGCCACTTATCGACACCTGAGGTTGG 522

```

```

RESULT 8
AM736058/c 534 bp mRNA EST 07-SEP-2000
LOCUS AM736058
DEFINITION EST332044 KV3 Medicago truncatula cDNA clone PKV3-503, mRNA
sequence.
ACCESSION AM736058
VERSION AM736058.1 GI:7642902
KEYWORDS EST.
SOURCE barrel medic.
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionidene; Medicago.
1 (bases 1 to 534)
REFERENCE
AUTHORS Vandenbosch, K., Hurt, J., Moore, J., Beremand, P., Peng, H., Ellis, L.,
Town, C.D., Bowman, C.L., Craven, M.B., Hansen, T.S., Holt, I.E. and
Fraser, C.M.
TITILE ESTs from roots of Medicago truncatula after Rhizobium inoculation
JOURNAL Unpublished (1999)
COMMENT Contact: Vandenbosch K
Department of Biology
Texas A&M University
College Station, TX 77843-3258, USA
Tel: 409 845 7707
Fax: 409 845 2891
Email: kate@mail.bio.tamu.edu
Texas A&M EST name: T254173e
TIGR sequence name: MTEA86TK
More information is available at:
'http://chrysis.tamu.edu/medicago/
Seq primer: SKmod (CTA gaa cta gtc gat cc).

```

```

FEATURES
source 1..534
Location/Qualifiers
/organism="Medicago truncatula"
/cultivar="genotype A17"
/db_xref="taxon:3880"
/clone="PKV3-503"
/clone_id="KV3"
/tissue_type="Seedling roots"
/dev_stage="3 days post-inoculation with Sinorhizobium
melliottii"
/lab_host="E. coli strain XL0LR"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XL0LR cells."

```

```

BASE COUNT 142 a 133 c 86 g 173 t
ORIGIN

```

```

Query Match 6.1%; Score 105.6; DB 120; Length 534;
Best Local Similarity 60.4%; Pred. No. 1.7e-14;
Matches 174; Conservative 0; Mismatches 114; Indels 0; Gaps 0;

```

```

Oy 977 aggttaagtcatagaaccctaaattgttacaatcgaggaaggaagcaatcatatc 1036
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 534 ATGTTAAGACCTTTAATCAAACTTGTACAGTTGTGAACAAGACGTGAACAACAAC 475

Oy 1037 catcctcttctttaaagaattcatcgagcgcttgatattatacagctgtgttgat 1096
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 474 ACTGCCCATTTCTTCCAAAGATTTGTGAAGCTTACATTTACTCTGCTGTGTTGAG 415

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FEATURES

Email: debbys@pucicni.crl.unn.edu
University of Minnesota name: M278413e
TIGR sequence name: MTFD8947K
More information is available at: <http://chrysle.tamu.edu/medicago>
Seq primer: SKm0d (CPA GAA CTA gta gat CC).
Location/Qualifiers

	Query Match	Similarity	Score	ID	Length
Best Local	188	55.9%	104.4	150	608
Matches	188	Conservative	0	Mismatches	156
				Indels	0
				Gaps	0

[illegible]

CONTRIBUTORS
 Oryzopsis, *maia*
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons: core eudicots;
 Rosidae; eustosids I; Fabales; Fabaceae; Papilionoideae; Glycine.
 I (bases 1 to 469)
 REFERENCE
 Shoemaker, R., Keim, P., Vocklin, L., Erpding, J., Corvelli, V., Khanna
 A., Boller, P., Maier, M., Müller, F., Frutcha, W., Martin, I., Beck, C.

TITLE	JOURNAL	COMMENT
Public Soybean EST Project	Unpublished (1999)	Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project		Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA		
Tel: 314 286 1800		
Fax: 314 286 1810		
Email: est@watson.wustl.edu		
This clone is available through: Genome Systems, Inc. 4633 World		
Parway Circle St. Louis, Missouri 63134 For further information		
call: (800) 430-0030 or (314) 427-3222 FAX: (888) 919-3324 or (314)		
427-3324 or contact: clones@genomesystems.com or		
info@genomesystems.com web site: www.genomesystems.com		
Insert length: 674 Std Error: 0.00		
High quality sequence strop: 386.		
Location/Qualifiers		
1..463		

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/organism="Glycine max"
/jb.xref="taxon:3847"
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/clone_1lb="Gm-cl016"
/tissue_type="Immature flowers of field grown plants"
/lib_host="Xl10-Gold"
/notice="Vector: plasmidscript II XR; Site 1: EcoRI; Site 2:
XhoI; This cDNA library was constructed from mRNA isolated
from immature flowers of field grown plants. The cDNA
library was prepared using the Stratagene Plasmidscript II
XR library construction kit. Complementary DNA was
synthesized from mRNA using a primer consisting of a poly
(dI) sequence with a XhoI restriction site. EcoRI adapted
fragments were ligated into the EcoRI-XhoI restriction site of the
plasmidscript vector. The ligated cDNA fragments were
transformed into Xl10-Gold cells. This library was
constructed by Dr Randy Shoemaker and Dr. John

```

BASE COUNT	134 a	97 c	118 g	120 t	Erpelding."
ORIGIN					
Query Match		5.9%	Score 102:	DB 24:	Length 469;
Best Local Similarity		57.5%	Pred. No. 1.2e-13;		
Matches 183;	Conservative	0;	Mismatches 135;	Indels	0;
				Gaps	0;
QY	669	ttttgcataaggttaagtcataatgaacccttaaatgttacaatcgcgcgaagaagca	1028		
DB	77	TTTTGAGATTTGGTAAAGTCACCTTCTCCCAAGGTACCCATTGGTGGAGCAATCA	136		
QY	1029	atcataaccatccctttttttaaagaatcattcgcagcgttgattattacagctg	1088		
DB	137	ACACAAACACAAACCCCTTCTTCAACAGGTCATTGAAACCTTGATTACTTGCCAA	196		
QY	1089	tgttgattcactgtaagctacatgcccgcgcggtagtcgagaaggatgacaattgaac	1148		
DB	197	TTTGTGAGTTCACATTAATGTCACCTCCCAAGACGACAGAGAGAGATTAATGTGGAC	256		
QY	1149	aagtgctggtttggaagagatctgtgatcgttgcgcgtggaagagataaagaag	1208		
DB	257	AACATTGCTGGCCAGGGATATTGCAATATCATTTGCTGTGAAGGCAAGAAAGGTTG	316		
QY	1209	aaagcactgaaaggtttagatcattggaagattgcttgaggagctgtgattagtaacg	1268		
DB	317	AGAGACATGACAACTGTCGGCAAGTGGAATCAAGGTTAAAGATGCGCGCTTCACAGCAAT	376		
QY	1269	ttgccttaagccctttg 1286			
DB	377	GTTCCTTGAGTCTTATG 394			
RESULT 14					
LOCUS	AM102078	495 bp	mRNA	EST	17-JUL-2000
DEFINITION	sds22g03.y1 Gm-c1009 Glycine max cDNA clone GENOME SYSTEMS CLONE ID				
	Gm-c1009-941 5' similar to TR:023566 O23566 SCARECROW HOMOLOG. ;				
	mRNA sequence.				
ACCESSION	AM102078				
VERSION	AM102078.1	GI:6072691			
KEYWORDS	EST.				
SOURCE	soybean.				
ORGANISM	Glycine max				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
AUTHORS	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;				
	Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Glycine.				
	1 (bases 1 to 495)				
	Shoemaker,R., Kelm,P., Vodkin,L., Erpelding,J., Coryell,V., Khana				
	,A., Boll,B., Maria,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.				
	Wyllie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers				
	,Y., Person,B., Swaller,T., Gibbons,M., Page,D., Harvey,N., Schurk				
	,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann				
	,R., Waterston,R. and Wilson,R.				
	Public Soybean EST Project				
	Unpublished (1999)				
TITLE	Contact: Shoemaker R/Public Soybean EST Project				
JOURNAL	Public Soybean EST Project				
COMMENT	Washington University School of Medicine				
	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA				
	Tel: 314 286 1800				
	Fax: 314 286 1810				
	Email: est@watson.wustl.edu				
	This clone is available through: Genome Systems, Inc. 4633 World				
	Parkway Circle St. Louis, Missouri 63134 For further information				
	call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314)				
	427-3324 or contact: clones@genomesystems.com or				
	info@genomesystems.com web site: www.genomesystems.com				
	Insert length: 708 Std Error: 0.00				
	Seq primer: -40RP from Gibco				
	High quality sequence stop: 408.				
FEATURES	Location/Qualifiers				

Source	1. 495
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	/lab_host="XLI0-Gold"
	/note="vector: pBluescript II Xr; Site_1: EcoRI; Site_2: XhoI; The mRNA was isolated from entire roots of 2-month-old 'Williams' plants that were greenhouse grown in 5-gallon pots. To suppress nodulation, Black Gold All-purpose potting soil was supplemented with: 0.36g/L available phosphoric acid (P205), 20mg/L urea N, 0.16g/L S, 0.49mg/L B, 2.5mg/L Cu, 0.15g/L Fe, 13.5mg/L Mn, 0.26mg/L Mo, 14mg/L Zn, 20mg/L Ca, and the following nutrients in a slow-release form (Osmocote): 0.165g/L ammonia N, 0.185g/L nitrate N, 0.35g/L available phosphoric acid, and 0.35g/L soluble potash. No nodules were visible on the roots at harvest. Stratagene's cDNA Synthesis kit (catalog #200401) was used to synthesize the cDNA. First-strand synthesis was performed with 5'-methyl dCTP, hence the ligated cDNA is hemimethylated. Stratagene's first-strand synthesis primer was used (GAGAGACAGAGACAGACAGACTGATCTCAG(7)-18). After second-strand synthesis, the cDNA ends were 'polished' with clone Pfu DNA polymerase, ligated to EcoRI adapters, and phosphorylated. The XhoI site within the first-strand synthesis primer was restricted by digestion with XhoI; all XhoI sites in the cDNA would be protected by their hemimethylated status. The cDNA constructs were size-fractionated with a 400bp cutoff, using a SizeSep 400 Spin column from Pharmacia. The column eluent was then ligated into Stratagene's pBluescript II Xr Predigested vector (pBluescript II SK(+)) that had been digested with EcoRI and XhoI, and phosphorylated. Both the white and blue colonies appear to contain recombinant plasmids with cDNA inserts. This library was constructed by Dr. Paul Keim and Dr. Virginia Corvett."
BASE COUNT	138 a 101 c 128 g 128 t
ORIGIN	
Query Match	5.9%; Score 102; DB 111; Length 495;
Best Local Similarity	57.5%; Pred. No. 1.2e-13;
Matches 183; Conservative	0; Mismatches 135; Indels 0; Gaps 0;
QY 969	ttttgcatagaggttaagtaatgaaccccaaaattgttacaatcgcgagaagaa 1028
DB 101	TTTTTGAGATTGGTAAAGGTACTTTCTCCCAAGGTGCCACATTGGTGCGAGATCA 160
QY 1029	atcataacatcctcttttttcaaaagattcatcgagcggttgattatlaaagct 1088
DB 161	ACACAACACAAACCCCTTTCTTCAACAGGTCAATGAACCTTGGATTCTCACTGGCA 220
QY 1089	tgttgattcaactgaagatcaatgcccacgggtagtcgagagaagatgacgttgaa 1148
DB 221	TCTTTGAGTCCATTGTATGTCCACCTCCCAAGACGACGACGAAGAGATTATGTGGAC 280
QY 1149	aagtggtggttggaagagatgttgatatacgtttcgattgaaagagaataaagaag 1208
DB 281	AACATTGTCTGGCCAGGGAATTGTCAATATATCTTGTGAAGGCAAGAAAGGCTTG 340
QY 1209	aaagacatgaaggtttatagatcatcggaagattatgttgagagatttgattaa 1268
DB 341	AGAGACATGATACGTTCGGCAAGTGAAGTAACGAAGTTAAAGTGGCGGCTTCCAGCAAT 400
QY 1269	ttgctttaagccctttg 1286
DB 401	gttcctttgagttctatg 418

DEFINITION	sd47d04.yl Gm-cl016 glycine max cDNA clone GENOME SYSTEMS CLONE ID: GM-cl016-2912 5' similar to TR:023566 023566 SCARCEBROW HOMOLOG. ;					
ACCESSION	AM119464					
VERSION	AM119464.1 GI:6094850					
KEYWORDS	EST.					
SOURCE	soybean. Glycine max Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatopsida; Magnoliophytes; eudicotyledons; core eudicots; Kosiidae; eucosids I; Fabales; Fabaceae; Papilionoideae; Glycine.					
ORGANISM	I (bases 1 to 497) Shoemaker,R., Keim,P., Vodkin,L., Erpelting,J., Corvelli,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kueba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Stepleok,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Page,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R. Public Soybean EST Project Unpublished (1999) Contact: Shoemaker R/Public Soybean EST project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available through: Genome Systems, Inc. 4633 World Parkway Circle St. Louis, Missouri 63114 For further information call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314) 427-3324 or contact: clones@genomesystems.com or info@genomesystems.com web site: www.genomesystems.com Insert Length: 657 Std Error: 0.00 Seq primer: -40RP from Gibco High quality sequence stop: 410. Location/Qualifiers 1..497 /organism="Glycine max" /db_xref="taxon:3847" /clone="GENOME SYSTEMS CLONE ID: Gm-cl016-2912" /clone_1lb="Gm-cl016" /tissue_type="Immature flowers of field grown plants" /lab_host="Xl10-Gold" /note="Vector: pluescript II XR; Site.1: EcoRI; Site.2: XhoI; This cDNA library was constructed from mRNA isolated from immature flowers of field grown plants. The cDNA library was prepared using the Stratagene pluescript II XR library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly (dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pluescript vector. The ligated cDNA fragments were transformed into Xl10-gold host cells. This library was constructed by Dr. Randy Shoemaker and Dr. John Erpelting."					
BASE COUNT	142 a 98 c 127 g 129 t 1 others					
ORIGIN						
Query Match	5.9%; Score 102; DB 111; Length 497;					
Best Local Similarity	57.5%; Pred.No.1.2e-13;					
Matches 183; Conservative	0; Mismatches 135; Indels 0; Gaps 0;					
QY 969	tttgcatagggttaagtcaatgaacccctaattgcttacatcgcgagaagaaacaa 1028					
	TTTTGGATTGGTGAAGGTACTTTCTCCCAAGTGACCACTGTGTGGTAGCAGGAATCAA 124					
Db 65						
QY 1029	atcataaccatccctctttttacaagaattcatcgaggcgtygatattatatcacgcty 1088					
Db 125	ACACAACACAAACCCTTTCTTCACAGAGGTTCATGAACACCTTGATTACTTGCGCAA 184					

QY	1089	tggttgattcaatgtagagcttaacttgcacccgggtatgcagtagagagatgacgttgaac	1148
Db	185	tcttttgatgccattgtagtgcacccctcccaagacacgcacagcagcaggttaattgtggagcc	244
QY	1149	aagcgttgatttggagagagagatctgtacatcgttgcagtgaagagataaagaagaa	1208
Db	245	amcattgtctggccacgagatattgtcaattatctcttgttaagcacaaggaaagggttg	304
QY	1209	aaagacatgaaaggctttaagatcatatgggaagtctgtctggagaggttctgtattagtaatg	1268
Db	305	agagacacatgaactcttttggcgaagcgaagtcacaaaggttaaaagatggccgcttcacagcaat	364
QY	1269	tgtcttaagccctttcg	1286
Db	365	gtccctttgagttcttatng	382

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